(MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 09:23:39 2000; MasPar time 83.13 Seconds 16.486 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-09-331-631-1 (29-73) from US09331631.pep (2 of 5) 361

1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 45

Scoring table: PAM 150 Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Mean 34.353; Variance 52.501;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.654

SUMMARIES

21 22 23	19 20	18	16	, ₁₁	12 13	11	10	. 9	·æ	7	σ	ر. د	4	ω	2	_	Result
71 71 71	72 72	73	73	73	73 73	74	74	. 75	77	77	94	95	95	100	101	115	Score
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Query Match 31.9%; Best Local Similarity 31.7%; Matches 13; Conservative

Score 115; DB 1; Length 588; Pred. No. 2.20e-08; 13; Mismatches 12; Indels

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Gaps

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CHD1_MOUSE TRMU_CHLPN KITH_ILTVT	STC_DROME FAS_CHICK D111_ARATH SG1_BOVIN	PTN2_RAT PTN2_MOUSE YEBS_ECOLI FIBA_CHICK	MAZ4_SCHCO VIT2_CAEEL MBP1_MAIZE Z155_HUMAN HM14_CAEEL	LAC2_NEUCR ATI1_VARV SEC3_YEAST: NXB2_CERLA YL53_CAEEL
DNA LIGASE (EC 6.5.1.2 CHROMODOMAIN-HELICASE- PROBABLE TRNA (5-METHY THYMIDINE KINASE (EC 2		PROTEIN-TYROSINE PHOSP PROTEIN-TYROSINE PHOSP HYPOTHETICAL 48.3 KD P FIBRINOGEN ALPHA/ALPHA	MATING-TYPE PROTEIN A- VITELLOGENIN 2 PRECURS ANTIMICROBIAL PEPTIDE ZINC FINGER PROTEIN 15 HOMEOBOX PROTEIN CEH-1	LACCASE PRECURSOR (EC 81 KD A-TYPE INCLUSION EXOCYST COMPLEX COMPON NEUROTOXIN B-II. HYPOTHETICAL 29.0 KD P
8.43e+00 8.43e+00 1.19e+01 1.19e+01	5.93e+00 5.93e+00 8.43e+00 8.43e+00	5.93e+00 5.93e+00 5.93e+00 5.93e+00	4.15e+00 4.15e+00 5.93e+00 5.93e+00 5.93e+00	2.89e+00 2.89e+00 2.89e+00 2.89e+00 4.15e+00 4.15e+00

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SEQUENCE 588 AA; 69729 MW;	CHAIN 26 588 VICILIN C72.	SIGNAL 1	Seed storage protein	PRAM; PROUD46; SeedSto		HSSP: P50477	PIR:	EMBL; M16891; AAA33071.1;		or send an email to license@isb-sib.ch).	entities requires a license agreement (See http://w	modified and this statement is not removed. Usage by and for	use by non-profit institutions as long as its	the European Bioinformatics Institute. There are no restrictions on its		This SWISS-PROT entry is copyright. It is produced through a collaboration		CONVICILIN, CONGLYCININ, ETC.).	-!- SIMILARITY:	BODIES.	-!- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN		Plant Mol. Biol. 7:475-489(1	the storage protein families.";	germination. XVIII. cDNA and amino acid sequences of the	"Developmental biochemistry of cottonseed			[1]					VICILIN C72 PRECURSOR (ALPHA-GLOBULIN	15-JUL-1999 (Rel. 38, Last	01-MAR-1989 (Rel. 10,	01-MAR-1989 (Rel.	P09801;	VCLB_GOSHI STANDARD; PRT; 588 AA.	RESULT 1

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DRQEYEECKRQCMQLETSGQMRR-CVSQCDKRFEEDIDWSK 71

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Ol-MAR-1989 (Rel. 10, Last sequence update)
15-UIL-1989 (Rel. 38, Last annotation update)
15-UIL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
Gossypium hirsutum (Upland cotton).
Gossypium hirsutum (Upland cotton).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; eudicotyledons;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
euphyllophytes; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium
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P56568;
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or send a
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-i- FUNCTION: SEED STORAGE PROTEIN.
-i- SUBCELLULAR LOCATION: COTYLEDONARY MEI
                                                                                                                              Luffa cylindrica (Smooth loofah) (Sponge gourd).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
                                           MEDLINE; 97357433.
Kimura M., Park S.S.,
                                                                                                                                                                                                      15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
Biosci.
             "Primary structure of
the seeds of sponge go
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Chlan C.A., Borrot
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KD ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.
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39.0%;
 ., Sakai R., Yamasaki N., Funats
of 6.5k-arginine/glutamate-rich
gourd (Luffa cylindrica).";
Biochem. 61:984-988(1997).
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Pred. No. 1.36e-05;
12; Mismatches 9
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P07996;
01-AUG-1988 (Rel. C
01-AUG-1988 (Rel. C
01-OCT-1996 (Rel. 3
THROMBOSPONDIN 1 PR
                                                                                                          gene. DN
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Dixit V.M.,
                                                                                                                                                                                                                                                                                                                                                                                     proteins.";
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Submitted (XXX-1992) to
                                                                                                                                                                                                                            Proc.
                                                                                                                                                                                                                                    Dixit V.M., Hennessy S.W., Grant G.A., Ro "Characterization of a cDNA encoding the domains of human thrombospondin."; Proc. Natl. Acad. Sci. U.S.A. 83:5449-545
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proteins.";
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                                                                                                          Laherty C.D., Glerman T.M., Dixit V.M., Characterization of the promoter region of gene. DNA sequences within the first intron J. Biol. Chem. 264:11222-11227(1989).
                                                                                                                                                                SEQUENCE OF 1-166 FROM N.A. MEDLINE; 89291870.
Laherty C.D., Glerman T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-397
MEDLINE; 87157592
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PFAM; PF00093; vwc; 1.
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EMBL; X04665; CAA28370.1; -
EMBL; X14787; CAA32889.1; -
EMBL; J04835; AAA61178.1; -
EMBL; M99425; AAA65281; -
PIR; A05172; A05172.
PIR; A55812; A25812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN.
SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEAT.
(WHICH BIND CALCIUM).
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A34274; A34274.
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FALSE_NEG.
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                                            TSP TYPE-1 1.

TSP TYPE-1 2.

TSP TYPE-1 3.

EGF-LIKE 1.

EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.)

TSP TYPE-3 1.

TSP TYPE-3 2.

TSP TYPE-3 3.

TSP TYPE-3 5.

TSP TYPE-3 6.

TSP TYPE-3 6.

TSP TYPE-3 7.

CELL ATTACHMENT SITE (POTENTIAL).

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.
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3 X EGF TYPE REPEATS.
7 X TSP TYPE-3 REPEATS.
C-TERMINAL.
-- ~vpn-1 1.
POTENTIAL.
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HEPARIN-BINDING (POTENTIAL).
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                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use: by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euriheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-JUN-1994 (Rel. 29, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
THROMBOSPONDIN 1 PRECURSOR.
THBS1 OR TSP1.
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-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRON
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Laherty C.D., O'Rourke
Dixit V.M.;
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                                                                                                                                                                                                                                                                                                                                                         LAMININ AND TYPE V COLLAGEN.
SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISUI
SIMILARITY: BELONGS TO THE THROMBOSPONDIN
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS
(WHICH'BIND CALCIUM).
M62470; AAA50611.1; M62450; AAA50611.1; M62451; AAA50611.1; M62452; AAA50611.1; M62453; AAA50611.1; M62453; AAA50611.1; M62454; AAA50611.1; M62455; AAA50611.1; M62455; AAA50611.1;
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3 X TSP TYPE-REPEATS.
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mitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ADHESTUE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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PIR; JQ1730; JQ1...
HSSP; P50477; 1CAW.
PFAM; PF00546; Seedstore_7s; 1
PFAM; PF00546; Sugar transport; S.
Transport; Sugar 29
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-!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.

-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.

-!- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.

-!- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER FERTILIZATION, NO DAYS AFTER FERTILIZATION, NO DAYS AFTER FERTILIZATION, NO DAYS AFTER FERTILIZATION, NO EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
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                                                                                                                                                                                                                 use by non-
modified and
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PEAM; PF00008; EG; , PFAM; PF00008; tsp_1; 3.
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Genomics 12:421-429(1992).

-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO
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SEQUENCE
                                                                                                                                                                                                                                                    PROSITE; PS00022; EGF_1; PROSITE; PS01186; EGF_2; PROSITE; PS01208; VWFC;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L12350;
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01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 49.6 KD PROTEIN C13D6.01 IN CHROMOSOME
            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENT EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 7.
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77;
Pred. No.
3; Misma
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INTERCHAIN (PROBABLE).
BY SIMILARITY.
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3 X EGF-TYPI
7 X TSP TYPI
C-TERMINAL.
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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EGF-TYPE REPEATS.
TSP TYPE-3 REPEATS (CA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   77; DB 1;
No. 3.08e-01
                                                                                                                                                                                                                                                                                                               431 AA.
                         (See http://www.isb-sib.ch/announce/
                                              There are no rest
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                                     Usage
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                                                                                 collaboration -
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RESULT 10
ID CYSK_YEAST
AC P53206;
DT 01-OCT-1996
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Best Local S
Matches 1
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Best Local S
Matches 1
TSP2_BOVIN STAN
Q95116;
01-NOV-1997 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
THROMBOSPONDIN 2 PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z69725;
Hypothetical p
SEQUENCE 431
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PUTATIVE CYSTEINE SYNTHASE (EC 4.2.99.8) (O-ACETYLSERINE SULFHYDRYLASE) (C-ACETYLSERINE (THIOL)-LYASE) (CSASE).
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                              EMBL; 272797; PROSITE; PS009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- PATHWAY: CYSTEINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE
SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                              Pyridoxal phosphate
                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Lyase;
                                                                                                                                                                                                                                                                                                                                PFAM; PF00291; S_T_dehydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGR012W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 13:1077-1090(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rieger M., Brueckner M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C
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                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 FKPQTFDEFV-HCLA-RVRA-MKRLVSICSN-FDEEDNWN
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                                                                                                                                           DRQEY-EECKRQCMQLETSGQMRRCVSQCDKRFEEDIDW
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Similarity 30.0%;
12; Conservative
                                                                                                                                                                                                       Similarity 33.3%;
13; Conservative
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431 AA; '
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                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                1; CYS_SYNTHASE; 1.
S T dehydratase; 1.
. 35, Created)
. 38, Last sequence update)
. 38, Last annotation update)
PRECURSOR (CORTICOTROPIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota;
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                                                                                                                                                                                                                     20.5%;
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3 kilobases from
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                                                                                                                                                                                                                                                                    76C73396D77B69AC CRC64;
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d. No. 9.59e-01
Mismatches 1!
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No.
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rom Saccharomyces
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tent is in
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    PROTEIN)
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                                                                                                        REPEAT
REPEAT
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DOMAIN
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                                                                                                                                                                                                                                                    PFAM; PF00090; tsp_1; 3. 
PFAM; PF00093; vwc; 1. 
Glycoprotein; Cell adhesion; 
EGF-like domain; Signal.
                                                                                                  REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Verteb:
Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige J.J.;
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                                                                                                                                                                                                                                                                                                                    X96540;
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Pellerin
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, Mosher D., Chambaz E.M.,
) to the EMBL/GenBank/DDBJ
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                                TSP TYPE-1 2.
TSP TYPE-1 3.
EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTEN EGF-LIKE 3.
TSP TYPE-3 1.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 4.
TSP TYPE-3 6.
TSP TYPE-3 7.
CELL ATTACHMENT SITE (POTENTIAL).
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
INTERCHAIN (PROBY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                             Calcium-binding;
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                                                                                                                                                                                      TSP TYPE-1 REPEATS (CS-LIKE).
EGF-TYPE REPEATS.
TSP TYPE-3 REPEATS (CA-BINDING).
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                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                    3. H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Mammalia;
Pecora; Bovoidea; Bovi
                                                                                                                                   CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danik M.,
                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                             Heparin-binding; Repeat;
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Feige J.J.;
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 Query Match
Best Local Similarity
Matches 9; Conser
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Best Local
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                                         CARBOHYD
SEQUENCE
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Q14508;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-FEP-2000 (Rel. 39, Last annotation update)
MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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CARBOHYD
                                                                                            Signal; Glycoprotein SIGNAL 1
                                                                                                                PROSITE; PS00317; 4_DISULFIDE_CORE; PFAM; PF00095; wap; 2.
                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                        sequence homology to extracellular proteinase inhib Biol. Reprod. 45:350-357(1991).
-:- FUNCTION: POSSIBLE FUNCTION IN SPERM MATURATION
                                                             DOMAIN
                                                                                   CHAIN
                                                                                                                                     EMBL; A18924; CAA01433.1; HSSP; P19957; 1FLE.
                                                                         DOMAIN
                                                                                                                                                          EMBL; X63187; CAA44869.1; -.
                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                PREDOMINANTLY WITHIN THE DISTAL SECTIONS.
-!- SIMILARITY: TO WAP-TYPE 'FOUR-DISULFIDE CORE' PROTEINS
                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: SECRETED -!- TISSUE SPECIFICITY: EPITHELIAL
                                                                                                                                                                                                                                                                                                                                     Kirchhoff C., Habben L., Ivell R.,
"A major human epididymis-specific
                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92153963.
Kirchhoff C., Habben L.,
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=EPIDIDYMIS;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SECRETORY PROTEIN E4).
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                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates;
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5; Mismatc
Score 73;
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7; Misma
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 re 73; DB 1; Lo
d. No. 1.39e+00;
Mismatches 7
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ic cDNA encodes a protein v
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Best Local Similarity
Matches 9; Conser
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
11-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 38.6 KD PROTEIN.
Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
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P19297;
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ATT1 VACCV STANDARD; PRT; 724 AA.
P24759;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
94 KD A-TYPE INCLUSION PROTEIN (ATI).
"Isolation and characterization of modified 94-kDa inclusion protein. Virology 185:768-778(1991).
                                                                                       MEDLINE; 92074241.
de Carlos A., Paez E.;
                                                                                                              SEQUENCE FROM N.A. MEDLINE; 92074241.
                                                                                                                                                                                                                                                Amegadzie B.Y., Sisler *Frame-shift mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 91310644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus.
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Viruses; dsDNA viruses, no
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                                                                                                                                                                                                                                                                                                                          SEQUENCE
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"Identification, sequence, and expression of the gene encoding 35,000 subunit of the vaccinia virus DNA-dependent RNA polymera J. Biol. Chem. 266:13712-13718(1991).
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larity 32.1%;
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Pred. No. 1.39e+00;
9; Mismatches 8
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EMBL; M76371; AAA48275.1; -.
EMBL; X57318; CAA40574.1; -.
PIR; X57318; CAA40574.1; -.
PIR; A41701; WMVZ94.
PIR; S29908; S29908.
CONFLICT 587 588 K
                                                                                                                                                                                                                                                                                                                                                    Orthopoxviruses.";
J. Gen. Virol. 74:1679-1684(1993).
J. FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO THE ATI, AND BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
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ATI_CAMPC
Q05482;
Q1-FEB-1995
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CONFLICT
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01-FEB-1995 (Rel. 31, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
A-TYPE INCLUSION PROTEIN (ATI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meyer H., Rziha H.-J.; "Characterization of the gene encoding the A-type inclusion protein of camelpox virus and sequence comparison with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Viruses; dsDNA viruses, no R
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MISCELLANEOUS: A CHARACTERISTIC FEATURE OF
LARGE MASSES WITH NO SURROUNDING MEMBRANES
INFECTED CELLS.
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No. 1.39e+00;
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